

PATENT

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AMENDMENTS TO THE CLAIMS

The following listing of claims replaces all prior versions, and listings, of claims in this application.

Listing of Claims

1. (Previously presented) A composition comprising a protein in crystalline form, wherein the protein consists of SEQ ID NO:3, and wherein the protein crystal has a crystal lattice in a $P2_1$ space group and unit cell dimensions, $\pm 5\%$, of $a=121.53\text{\AA}$ $b=124.11\text{\AA}$ and $c=144.42\text{\AA}$, $\alpha=\gamma=90^\circ$, $\beta=114.6^\circ$.
- 2-3. (Canceled)
4. (Previously presented) A composition according to claim 1 wherein the protein crystal diffracts X-rays for a determination of structure coordinates to a resolution less than 3.0 Angstroms.
- 5-6. (Canceled)
7. (Previously presented) A method for forming a crystal of a protein comprising:
forming a crystallization volume comprising a precipitant solution and a protein that consists of SEQ ID NO:3, and wherein the protein crystal has a crystal lattice in a $P2_1$ space group and unit cell dimensions, $\pm 5\%$, of $a=121.53\text{\AA}$ $b=124.11\text{\AA}$ and $c=144.42\text{\AA}$, $\alpha=\gamma=90^\circ$, $\beta=114.6^\circ$; and
storing the crystallization volume under conditions suitable for crystal formation of the protein.
8. (Previously presented) A method according to claim 7 wherein is expressed from a nucleic acid molecule that comprises SEQ ID NO:2.
9. (Canceled)
10. (Previously presented) A method according to claim 7 wherein the protein crystal diffracts X-rays for a determination of structure coordinates to a resolution less than 3.0 Angstroms.
- 11-12. (Canceled)

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13. (Original) A method according to claim 7, the method further comprising diffracting the protein crystal to produce a diffraction pattern and solving the structure of the protein from the diffraction pattern.
14. (Canceled)
15. (Previously presented) A protein according to claim 16 where the protein is expressed from a nucleic acid molecule that comprises SEQ ID NO:2.
16. (Currently amended) A non-crystalline protein consisting of SEQ ID NO:3.
17. (Withdrawn) A method of identifying an entity that associates with a protein, comprising:
taking structure coordinates from diffraction data obtained from a protein crystal formed according to the method of claim 7; and
performing rational drug design using a three dimensional structure that is based on the obtained structure coordinates.
18. (Withdrawn) A method according to claim 17 wherein the protein from which the protein crystal is formed is expressed from a nucleic acid molecule that comprises SEQ ID NO:2.
19. (Canceled)
20. (Withdrawn) A method according to claim 17, the method further comprising selecting one or more entities based on the rational drug design and contacting the selected entities with the protein.
21. (Withdrawn) A method according to claim 17, the method further comprising measuring an activity of the protein when contacted with the one or more entities.
- 22-23. (Canceled)
24. (Currently amended) A non-crystalline protein consisting of residues 39-766 of SEQ ID NO:1.
- 25-26. (Canceled)

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27. (New) The protein according to claim 24 wherein the protein is expressed from a nucleic acid molecule that consists of SEQ ID NO:2.
28. (New) An isolated non-crystalline protein consisting of residues 39-766 of SEQ ID NO:1.
29. (New) An isolated non-crystalline protein consisting of SEQ ID NO:3.
30. (New) A composition comprising a protein in crystalline form wherein the protein consists of residues 39-766 of SEQ ID NO:1, and wherein the protein crystal has a crystal lattice in a $P2_1$ space group and unit cell dimensions, $\pm 5\%$, of $a=121.53\text{\AA}$ $b=124.11\text{\AA}$ and $c=144.42\text{\AA}$, $\alpha=\gamma=90^\circ$, $\beta=114.6^\circ$.
31. (New) A method comprising:
forming a crystallization volume comprising a precipitant solution and a protein that consists of residues 39-766 of SEQ ID NO:1, and wherein the protein crystal has a crystal lattice in a $P2_1$ space group and unit cell dimensions, $\pm 5\%$, of $a=121.53\text{\AA}$ $b=124.11\text{\AA}$ and $c=144.42\text{\AA}$, $\alpha=\gamma=90^\circ$, $\beta=114.6^\circ$; and
storing the crystallization volume under conditions suitable for formation of a protein crystal.